

Amendments to the Specification

Please replace the Sequence Listing on pages 1-9 as filed on June 4, 2004, with a substitute Sequence Listing presented on pages 1-24, enclosed herewith.

*KM
3/16/07*
On page 5, please replace the paragraph starting on line 4 with the following:

Fig. 1A-B. **Tat components of *B. subtilis* and *E. coli*.** The amino acid sequences of Tat components of *B. subtilis* and *E. coli* as deduced from the SubtiList (<http://bioweb.pasteur.fr/Genolist/SubtiList.html>) and Colibri (<http://bioweb.pasteur.fr/Genolist/Colibri.html>) databases were used for comparisons. Identical amino acids, or conservative replacements are marked. Putative transmembrane segments, indicated in gray shading, were predicted with the TopPred2 algorithm (34, 35) (A) Comparison of TatAc (YnzA, SEQ ID NO:5), TatAd (YczB, SEQ ID NO:4) and TatAy (Ydl, SEQ ID NO:3) of *B. subtilis* (Bsu) with TatA (SEQ ID NO:1), TatB (SEQ ID NO:6) and TatE of *E. coli* (Eco) (SEQ ID NO: 24-6). (B) Comparison of TatCd (YcbT, SEQ ID NO:9) and TatCy (YdiJ, SEQ ID NO:8) of *B. subtilis* with TatC of *E. coli* (SEQ ID NO: 7([-9])).

On page 7, please replace the paragraph starting on line 14 with the following:

Fig 7. **Predicted twin-arginine (RR-)signal peptides of *B. subtilis*.** The listed signal peptides contain, in addition to the twin-arginines, at least one other residue of the consensus sequence (R-R-X-ΦΦ; printed in bold). The number of residues in the N- and H-domains of each signal peptide, and the average hydrophobicity (h) of each of these domains, as determined by the algorithms of Kyte and Doolittle (Kyte, J., and R. F. Doolittle [1982] A simple method for displaying the hydropathic character of a protein. *J. Mol. Biol.* 157:105-32), are indicated. Furthermore, the RR-motifs in the N-domain, and SPase I recognition sites in the C-domain (ie. positions -3 to -1 relative to the predicted SPase cleavage site) are shown. Proteins lacking a (putative) SPase I cleavage site, some of which contain additional transmembrane domains, are indicated with "TM". One protein containing cell wall binding repeats is indicated with "W".

Please replace Table I and the text following the Table, on page 56 with the following: